

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: October 18, 2004, 22:46:12 ; Search time 128 Seconds
(without alignments)
1252.861 Million cell updates/sec

Title: US-10-600-689-4
Perfect score: 2612
Sequence: 1 MIDLKQYEFVFLVGSQYLYG.....LENFKKELRWNELYWGLLKR 496

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1360919 seqs, 323318874 residues
Total number of hits satisfying chosen parameters: 1360919

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA: *
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2612	100.0	496	14	US-10-193-896-12
2	2612	100.0	496	15	US-10-600-689-4
3	2508	96.0	496	14	US-10-193-896-11
4	2508	96.0	496	14	US-10-369-493-2914
5	1655	63.4	498	14	US-10-204-220-2
6	1653	63.3	497	14	US-10-193-896-6
7	1547	59.2	497	14	US-10-193-896-7
8	1547	59.2	497	14	US-10-369-493-17266
9	1443.5	55.3	500	14	US-10-193-896-4
10	1436.5	55.0	500	14	US-10-369-493-698
11	1434.5	54.9	500	14	US-10-193-896-3
12	1424.5	54.5	498	14	US-10-193-896-8
13	1424.5	54.5	498	14	US-10-369-493-23234
14	1315.5	50.4	501	14	US-10-193-896-13

15	1301	49.8	488	14	US-10-193-896-9	Sequence 9, Appli
16	1270	48.6	488	14	US-10-193-896-10	Sequence 10, Appl
17	1212.5	46.4	498	14	US-10-193-896-5	Sequence 5, Appli
18	389	14.9	465	14	US-10-193-896-2	Sequence 2, Appli
19	364.5	14.0	407	14	US-10-193-896-14	Sequence 14, Appl
20	131	5.0	958	14	US-10-216-682-9	Sequence 9, Appli
21	123.5	4.7	983	14	US-10-216-682-11	Sequence 11, Appl
22	117	4.5	982	15	US-10-456-129-12	Sequence 12, Appl
23	113.5	4.3	958	14	US-10-216-682-8	Sequence 8, Appli
24	112	4.3	608	15	US-10-282-122A-54351	Sequence 54351, A
25	111	4.2	949	15	US-10-456-129-11	Sequence 11, Appl
26	107.5	4.1	620	14	US-10-369-493-19442	Sequence 19442, A
27	107.5	4.1	828	14	US-10-369-493-3166	Sequence 3166, Ap
28	107.5	4.1	1831	16	US-10-437-963-126019	Sequence 126019,
29	106	4.1	551	14	US-10-314-657-70	Sequence 70, Appl
30	105.5	4.0	595	15	US-10-424-599-200624	Sequence 200624,
31	105.5	4.0	636	9	US-09-738-626-5590	Sequence 5590, Ap
32	105.5	4.0	636	16	US-10-781-014-404	Sequence 404, App
33	105	4.0	2167	9	US-09-778-927A-61	Sequence 61, Appl
34	105	4.0	2200	10	US-09-796-575-2	Sequence 2, Appli
35	105	4.0	2200	16	US-10-652-814-2	Sequence 2, Appli
36	105	4.0	2201	13	US-10-100-912-2	Sequence 2, Appli
37	105	4.0	2201	14	US-10-465-572-12	Sequence 12, Appl
38	105	4.0	2201	15	US-10-373-801-34	Sequence 34, Appl
39	104.5	4.0	641	15	US-10-282-122A-50915	Sequence 50915, A
40	103	3.9	539	14	US-10-156-761-9228	Sequence 9228, Ap
41	103	3.9	612	14	US-10-156-761-10209	Sequence 10209, A
42	103	3.9	872	13	US-10-047-260-38	Sequence 38, Appl
43	103	3.9	872	14	US-10-310-154-484	Sequence 484, App
44	103	3.9	872	14	US-10-369-493-2762	Sequence 2762, Ap
45	103	3.9	957	14	US-10-216-682-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-10-193-896-12
; Sequence 12, Application US/10193896
; Publication No. US20030129710A1
; GENERAL INFORMATION:
; APPLICANT: Biotechnologisk Institut
; APPLICANT: Jorgensen, Flemming
; APPLICANT: Hansen, Ole C.
; APPLICANT: Stougaard, Peter
; APPLICANT: Berthelsen, Hans
; APPLICANT: Eriknaer, Kristian
; APPLICANT: Bottcher, Karen
; APPLICANT: Christensen, Hans Jorgen Singel
; TITLE OF INVENTION: A novel thermostable isomerase and use
; TITLE OF INVENTION: hereof
; FILE REFERENCE: 30077US02
; CURRENT APPLICATION NUMBER: US/10/193,896
; CURRENT FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/305,155
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/905,108
; PRIOR FILING DATE: 2001-07-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 496
; TYPE: PRT
; ORGANISM: T.neapol
US-10-193-896-12

Query Match 100.0%; Score 2612; DB 14; Length 496;
Best Local Similarity 100.0%; Pred. No. 1.7e-220;
Matches 496; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MIDLKQYEFVFLVGSQYLYGLETLLKKVEQQASRIVEALNNDPIFFPSKIVLKPVLKNSAEI 60
Db 1 MIDLKQYEFVFLVGSQYLYGLETLLKKVEQQASRIVEALNNDPIFFPSKIVLKPVLKNSAEI 60

QY 61 REIFEKANAEPKAGVIVVMHTFSPSKMWIRGLSINKKPLLHLHTQYNREIPWDTIDMDY 120
Db 61 REIFEKANAEPKAGVIVVMHTFSPSKMWIRGLSINKKPLLHLHTQYNREIPWDTIDMDY 120
QY 121 MNLNQSAHGDRHGFIHARMRLPRKVVVGHWDREVREKIAKWMRVACAIQDGRGTQIVR 180
Db 121 MNLNQSAHGDRHGFIHARMRLPRKVVVGHWDREVREKIAKWMRVACAIQDGRGTQIVR 180
QY 181 FGNMREVASTEDDKVEAQIKLGWSINTWVGELAEAGVKAVPENEVEELLKEYKERYIMP 240
Db 181 FGNMREVASTEDDKVEAQIKLGWSINTWVGELAEAGVKAVPENEVEELLKEYKERYIMP 240
QY 241 EDEYSLKAIREQAQMEIALREFLKEKNAIAFTTTTFEDLHDLPLQLPGLAVQRLMEEGYGF 300
Db 241 EDEYSLKAIREQAQMEIALREFLKEKNAIAFTTTTFEDLHDLPLQLPGLAVQRLMEEGYGF 300
QY 301 AEGDWKAAAGLVRLKVMGAGLPGGTSFMEDYTYHLTPGNELVLGAHMLEVCPTIAKEKPR 360
Db 301 AEGDWKAAAGLVRLKVMGAGLPGGTSFMEDYTYHLTPGNELVLGAHMLEVCPTIAKEKPR 360
QY 361 IEVHPLSIGGKADPARLVFDQEGPAVNASIVDMGNRFRLLVNRVLSVPIERKMPKLPTA 420
Db 361 IEVHPLSIGGKADPARLVFDQEGPAVNASIVDMGNRFRLLVNRVLSVPIERKMPKLPTA 420
QY 421 RVLWKPLPDFKRATTAWILAGGSHHTAFSTAVDVEYLIDWAEALEIEYLVIDENLDLENF 480
Db 421 RVLWKPLPDFKRATTAWILAGGSHHTAFSTAVDVEYLIDWAEALEIEYLVIDENLDLENF 480
QY 481 KKELRWNELYWGLLKR 496
Db 481 KKELRWNELYWGLLKR 496

RESULT 2
US-10-600-689-4
; Sequence 4, Application US/10600689
; Publication No. US20040058419A1
; GENERAL INFORMATION:
; APPLICANT: PYUN, Yu Ryang
; APPLICANT: KIM, Byoung Chan
; APPLICANT: LEE, Han Seung
; APPLICANT: LEE, Dong Woo
; APPLICANT: LEE, Yoon Hee
; TITLE OF INVENTION: THERMOSTABLE L-ARABINOSE ISOMERASE AND
; TITLE OF INVENTION: PROCESS FOR PREPARING D-TAGATOSE
; FILE REFERENCE: LEELE81.001C1
; CURRENT APPLICATION NUMBER: US/10/600,689
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/KR01/02243
; PRIOR FILING DATE: 2001-12-22
; PRIOR APPLICATION NUMBER: KR2000/80711
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: KR2000/80608
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Thermotoga neapolitana 5068
US-10-600-689-4

Query Match 100.0%; Score 2612; DB 15; Length 496;
Best Local Similarity 100.0%; Pred. No. 1.7e-220;
Matches 496; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MIDLKQYEFWFLVGSQYLYGLETLLKKVEQQASRIVEALNNDPIFPFSKIVLKPVLKNSAEI 60
Db 1 MIDLKQYEFWFLVGSQYLYGLETLLKKVEQQASRIVEALNNDPIFPFSKIVLKPVLKNSAEI 60
QY 61 REIFEKANAEPKAGVIVVMHTFSPSKMWIRGLSINKKPLLHLHTQYNREIPWDTIDMDY 120

Db 61 REIFEKANAEPKAGVIVVMHTFSPSKMWIRGLSINKKPLLHLHTQYNREIPWDTIDMDY 120
QY 121 MNLNQSAHGDRHGFIHARMRLPRKVVVGHWDREVREKIAKWMRVACAIQDGRGTQIVR 180
Db 121 MNLNQSAHGDRHGFIHARMRLPRKVVVGHWDREVREKIAKWMRVACAIQDGRGTQIVR 180
QY 181 FGNMREVASTEDDKVEAQIKLGWSINTWVGELAEAGVKAVPENEVEELLKEYKERYIMP 240
Db 181 FGNMREVASTEDDKVEAQIKLGWSINTWVGELAEAGVKAVPENEVEELLKEYKERYIMP 240
QY 241 EDEYSLKAIREQAQMEIALREFLKEKNAIAFTTTTFEDLHDLPLQLPGLAVQRLMEEGYGF 300
Db 241 EDEYSLKAIREQAQMEIALREFLKEKNAIAFTTTTFEDLHDLPLQLPGLAVQRLMEEGYGF 300
QY 301 AEGDWKAAAGLVRLKVMGAGLPGGTSFMEDYTYHLTPGNELVLGAHMLEVCPTIAKEKPR 360
Db 301 AEGDWKAAAGLVRLKVMGAGLPGGTSFMEDYTYHLTPGNELVLGAHMLEVCPTIAKEKPR 360
QY 361 IEVHPLSIGGKADPARLVFDQEGPAVNASIVDMGNRFRLLVNRVLSVPIERKMPKLPTA 420
Db 361 IEVHPLSIGGKADPARLVFDQEGPAVNASIVDMGNRFRLLVNRVLSVPIERKMPKLPTA 420
QY 421 RVLWKPLPDFKRATTAWILAGGSHHTAFSTAVDVEYLIDWAEALEIEYLVIDENLDLENF 480
Db 421 RVLWKPLPDFKRATTAWILAGGSHHTAFSTAVDVEYLIDWAEALEIEYLVIDENLDLENF 480
QY 481 KKELRWNELYWGLLKR 496
Db 481 KKELRWNELYWGLLKR 496

RESULT 3
US-10-193-896-11
; Sequence 11, Application US/10193896
; Publication No. US20030129710A1
; GENERAL INFORMATION:
; APPLICANT: Biotechnologisk Institut
; APPLICANT: Jorgensen, Flemming
; APPLICANT: Hansen, Ole C.
; APPLICANT: Stougaard, Peter
; APPLICANT: Berthelsen, Hans
; APPLICANT: Eriknauer, Kristian
; APPLICANT: Bottcher, Karen
; APPLICANT: Christensen, Hans Jorgen Singel
; TITLE OF INVENTION: A novel thermostable isomerase and use
; TITLE OF INVENTION: hereof
; FILE REFERENCE: 30077US02
; CURRENT APPLICATION NUMBER: US/10/193,896
; CURRENT FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/305,155
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/905,108
; PRIOR FILING DATE: 2001-07-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 496
; TYPE: PRT
; ORGANISM: T.maritima
US-10-193-896-11

Query Match 96.0%; Score 2508; DB 14; Length 496;
Best Local Similarity 94.8%; Pred. No. 2.4e-211;
Matches 470; Conservative 18; Mismatches 8; Indels 0; Gaps 0;
QY 1 MIDLKQYEFWFLVGSQYLYGLETLLKKVEQQASRIVEALNNDPIFPFSKIVLKPVLKNSAEI 60
Db 1 MIDLKQYEFWFLVGSQYLYGLETLLKKVEQQASRIVEALNNDPIFPFSKIVLKPVLKNSAEI 60
QY 61 REIFEKANAEPKAGVIVVMHTFSPSKMWIRGLSINKKPLLHLHTQYNREIPWDTIDMDY 120
Db 61 TEIFEKANADPKAGVIVVMHTFSPSKMWIRGLSINKKPLLHLHTQYNREIPWDTIDMDY 120

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OM protein - protein search, using sw model

Run on: October 18, 2004, 22:42:57 ; Search time 467 Seconds
(without alignments)
1176.804 Million cell updates/sec

Title: US-10-600-689-4
Perfect score: 2612
Sequence: 1 MIDLKQYEFWFLVGSQYLYG.....LENFKKELRWNELYWGLLKR 496

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 6730630 seqs, 1107998698 residues

Total number of hits satisfying chosen parameters: 6730630

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents AA Main:
1: /cgn2_6/ptodata/1/paa/pctus COMB.pep.*
2: /cgn2_6/ptodata/1/paa/US06 COMB.pep.*
3: /cgn2_6/ptodata/1/paa/US07 COMB.pep.*
4: /cgn2_6/ptodata/1/paa/US08 COMB.pep.*
5: /cgn2_6/ptodata/1/paa/US081 COMB.pep.*
6: /cgn2_6/ptodata/1/paa/US082 COMB.pep.*
7: /cgn2_6/ptodata/1/paa/US083 COMB.pep.*
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9: /cgn2_6/ptodata/1/paa/US085 COMB.pep.*
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14: /cgn2_6/ptodata/1/paa/US090 COMB.pep.*
15: /cgn2_6/ptodata/1/paa/US091 COMB.pep.*
16: /cgn2_6/ptodata/1/paa/US092 COMB.pep.*
17: /cgn2_6/ptodata/1/paa/US093 COMB.pep.*
18: /cgn2_6/ptodata/1/paa/US094 COMB.pep.*
19: /cgn2_6/ptodata/1/paa/US095 COMB.pep.*
20: /cgn2_6/ptodata/1/paa/US096 COMB.pep.*
21: /cgn2_6/ptodata/1/paa/US097A COMB.pep.*
22: /cgn2_6/ptodata/1/paa/US097B COMB.pep.*
23: /cgn2_6/ptodata/1/paa/US098 COMB.pep.*
24: /cgn2_6/ptodata/1/paa/US099A COMB.pep.*
25: /cgn2_6/ptodata/1/paa/US099B COMB.pep.*
26: /cgn2_6/ptodata/1/paa/US100 COMB.pep.*
27: /cgn2_6/ptodata/1/paa/US101 COMB.pep.*
28: /cgn2_6/ptodata/1/paa/US102 COMB.pep.*
29: /cgn2_6/ptodata/1/paa/US103 COMB.pep.*
30: /cgn2_6/ptodata/1/paa/US104 COMB.pep.*
31: /cgn2_6/ptodata/1/paa/US105 COMB.pep.*
32: /cgn2_6/ptodata/1/paa/US106 COMB.pep.*
33: /cgn2_6/ptodata/1/paa/US107 COMB.pep.*
34: /cgn2_6/ptodata/1/paa/US108 COMB.pep.*
35: /cgn2_6/ptodata/1/paa/US109 COMB.pep.*
36: /cgn2_6/ptodata/1/paa/US60 COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

*

Result No.	Score	Query Match	Length	DB	ID	Description
1	2612	100.0	496	27	US-10-193-896-12	Sequence 12, Appl
2	2612	100.0	496	32	US-10-600-689-4	Sequence 4, Appl
3	2508	96.0	496	27	US-10-193-896-11	Sequence 11, Appl
4	2508	96.0	496	29	US-10-369-493-2914	Sequence 2914, Ap
5	2508	96.0	496	36	US-60-360-039-2914	Sequence 2914, Ap
6	1655	63.4	498	28	US-10-204-220-2	Sequence 2, Appl
7	1653	63.3	497	27	US-10-193-896-6	Sequence 6, Appl
8	1547	59.2	497	27	US-10-193-896-7	Sequence 7, Appl
9	1547	59.2	497	29	US-10-369-493-17266	Sequence 17266, A
10	1547	59.2	497	36	US-60-360-039-17266	Sequence 17266, A
11	1456.5	55.8	597	30	US-10-446-203-12394	Sequence 12394, A
12	1443.5	55.3	500	27	US-10-193-896-4	Sequence 4, Appl
13	1440.5	55.1	506	16	US-09-252-691-9419	Sequence 9419, Ap
14	1440.5	55.1	506	16	US-09-252-691C-9419	Sequence 9419, Ap
15	1440.5	55.1	506	30	US-10-417-886-9419	Sequence 9419, Ap
16	1436.5	55.0	500	29	US-10-369-493-698	Sequence 698, App
17	1436.5	55.0	500	36	US-60-360-039-698	Sequence 698, App
18	1434.5	54.9	500	27	US-10-193-896-3	Sequence 3, Appl
19	1424.5	54.5	498	27	US-10-193-896-8	Sequence 8, Appl
20	1424.5	54.5	498	29	US-10-369-493-23234	Sequence 23234, A
21	1424.5	54.5	498	36	US-60-360-039-23234	Sequence 23234, A
22	1315.5	50.4	501	27	US-10-193-896-13	Sequence 13, Appl
23	1301	49.8	488	27	US-10-193-896-9	Sequence 9, Appl
24	1270	48.6	488	27	US-10-193-896-10	Sequence 10, Appl
25	1245	47.7	479	30	US-10-417-884-6017	Sequence 6017, Ap
26	1245	47.7	479	30	US-10-417-884A-6017	Sequence 6017, Ap
27	1212.5	46.4	498	27	US-10-193-896-5	Sequence 5, Appl
28	389	14.9	465	24	US-09-905-108-2	Sequence 2, Appl
29	389	14.9	465	27	US-10-193-896-2	Sequence 2, Appl
30	364.5	14.0	407	27	US-10-193-896-14	Sequence 14, Appl
31	310.5	11.9	108	23	US-09-865-590A-20004	Sequence 20004, A
32	137	5.2	471	15	US-09-103-611D-21	Sequence 21, Appl
33	131	5.0	958	19	US-09-506-153-9	Sequence 9, Appl
34	131	5.0	958	28	US-10-216-682-9	Sequence 9, Appl
35	123.5	4.7	983	19	US-09-506-153-11	Sequence 11, Appl
36	123.5	4.7	983	28	US-10-216-682-11	Sequence 11, Appl
37	118.5	4.5	449	1	PCT-US03-13699-369	Sequence 369, App
38	117	4.5	982	30	US-10-456-129-12	Sequence 12, Appl
39	117	4.5	1481	22	US-09-791-537-87117	Sequence 87117, A
40	113.5	4.3	958	19	US-09-506-153-8	Sequence 8, Appl
41	113.5	4.3	958	28	US-10-216-682-8	Sequence 8, Appl
42	112	4.3	608	22	US-09-791-537-20913	Sequence 20913, A
43	112	4.3	608	28	US-10-282-122A-54351	Sequence 54351, A
44	111	4.2	949	30	US-10-456-129-11	Sequence 11, Appl
45	109.5	4.2	925	30	US-10-425-115-231646	Sequence 231646,

ALIGNMENTS

RESULT 1
US-10-193-896-12
; Sequence 12, Application US/10193896
; GENERAL INFORMATION:
; APPLICANT: Biotechnologisk Institut
; APPLICANT: Jorgensen, Flemming
; APPLICANT: Hansen, Ole C.
; APPLICANT: Stougaard, Peter
; APPLICANT: Berthelsen, Hans
; APPLICANT: Eriknaer, Kristian
; APPLICANT: Bottcher, Karen
; APPLICANT: Christensen, Hans Jorgen Singel
; TITLE OF INVENTION: A novel thermostable isomerase and use
; TITLE OF INVENTION: hereof
; FILE REFERENCE: 30077US02
; CURRENT APPLICATION NUMBER: US/10/193,896
; CURRENT FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/305,155
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/905,108


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; PRIOR FILING DATE: 2001-07-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 496
; TYPE: PRT
; ORGANISM: T.neapol
US-10-193-896-12

Query Match          100.0%; Score 2612; DB 27; Length 496;
Best Local Similarity 100.0%; Pred. No. 6.3e-246;
Matches 496; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIDLKQYEFWFLVGSQYLYGLETLLKKVEQQASRIVEALNNDPIPPSKIVLKPVLKNSAEI 60
Db 1 MIDLKQYEFWFLVGSQYLYGLETLLKKVEQQASRIVEALNNDPIPPSKIVLKPVLKNSAEI 60

QY 61 REIFEKANAEPCAGVIVWMHTFSPSKMWIRGLSINKKPLLHLHTQYNREIPWDTIDMDY 120
Db 61 REIFEKANAEPCAGVIVWMHTFSPSKMWIRGLSINKKPLLHLHTQYNREIPWDTIDMDY 120

QY 121 MNLNQSAHGDRHGFHARMRLPRKVVVGHWDREVEKEIAKWMRVACAIQDGRGTQIVR 180
Db 121 MNLNQSAHGDRHGFHARMRLPRKVVVGHWDREVEKEIAKWMRVACAIQDGRGTQIVR 180

QY 181 FGDNRREVASTEDDKVEAQIKLGSINTWGVGELAEGVKA VPENEVEELLKEYKERYIMP 240
Db 181 FGDNRREVASTEDDKVEAQIKLGSINTWGVGELAEGVKA VPENEVEELLKEYKERYIMP 240

QY 241 EDEYSLKAIREQAKMEIALREFLKEKNAIAFTTTFFEDLHDLPLQLPGLAVQRLMEEGYGFG 300
Db 241 EDEYSLKAIREQAKMEIALREFLKEKNAIAFTTTFFEDLHDLPLQLPGLAVQRLMEEGYGFG 300

QY 301 AEGDWKAAAGLVRLKVMGAGLPGGTSFMEDYTYHLTPGNELVLGAHMLEVCPTIAKEKPR 360
Db 301 AEGDWKAAAGLVRLKVMGAGLPGGTSFMEDYTYHLTPGNELVLGAHMLEVCPTIAKEKPR 360

QY 361 IEVHPLSIGGKADPARLVFDQEGPAPVNASIVDMGNRFRLLVNRVLSVPIERKMPKLPTA 420
Db 361 IEVHPLSIGGKADPARLVFDQEGPAPVNASIVDMGNRFRLLVNRVLSVPIERKMPKLPTA 420

QY 421 RVLWKPLPDFKRATTAWILAGGSHHTAFSTAVDVEYLIDWAEALEIEYLVIDENLDLENF 480
Db 421 RVLWKPLPDFKRATTAWILAGGSHHTAFSTAVDVEYLIDWAEALEIEYLVIDENLDLENF 480

QY 481 KKELRWNELYWGLLKR 496
Db 481 KKELRWNELYWGLLKR 496
```

```

RESULT 2
US-10-600-689-4
; Sequence 4, Application US/10600689
; GENERAL INFORMATION:
; APPLICANT: PYUN, Yu Ryang
; APPLICANT: KIM, Byoung Chan
; APPLICANT: LEE, Han Seung
; APPLICANT: LEE, Dong Woo
; APPLICANT: LEE, Yoon Hee
; TITLE OF INVENTION: THERMOSTABLE L-ARABINOSE ISOMERASE AND
; FILE REFERENCE: LEELE81.001C1
; CURRENT APPLICATION NUMBER: US/10/600,689
; CURRENT FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/KR01/02243
; PRIOR FILING DATE: 2001-12-22
; PRIOR APPLICATION NUMBER: KR2000/80711
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: KR2000/80608
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
```

```

; LENGTH: 496
; TYPE: PRT
; ORGANISM: Thermotoga neapolitana 5068
US-10-600-689-4

Query Match          100.0%; Score 2612; DB 32; Length 496;
Best Local Similarity 100.0%; Pred. No. 6.3e-246;
Matches 496; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIDLKQYEFWFLVGSQYLYGLETLLKKVEQQASRIVEALNNDPIPPSKIVLKPVLKNSAEI 60
Db 1 MIDLKQYEFWFLVGSQYLYGLETLLKKVEQQASRIVEALNNDPIPPSKIVLKPVLKNSAEI 60

QY 61 REIFEKANAEPCAGVIVWMHTFSPSKMWIRGLSINKKPLLHLHTQYNREIPWDTIDMDY 120
Db 61 REIFEKANAEPCAGVIVWMHTFSPSKMWIRGLSINKKPLLHLHTQYNREIPWDTIDMDY 120

QY 121 MNLNQSAHGDRHGFHARMRLPRKVVVGHWDREVEKEIAKWMRVACAIQDGRGTQIVR 180
Db 121 MNLNQSAHGDRHGFHARMRLPRKVVVGHWDREVEKEIAKWMRVACAIQDGRGTQIVR 180

QY 181 FGDNRREVASTEDDKVEAQIKLGSINTWGVGELAEGVKA VPENEVEELLKEYKERYIMP 240
Db 181 FGDNRREVASTEDDKVEAQIKLGSINTWGVGELAEGVKA VPENEVEELLKEYKERYIMP 240

QY 241 EDEYSLKAIREQAKMEIALREFLKEKNAIAFTTTFFEDLHDLPLQLPGLAVQRLMEEGYGFG 300
Db 241 EDEYSLKAIREQAKMEIALREFLKEKNAIAFTTTFFEDLHDLPLQLPGLAVQRLMEEGYGFG 300

QY 301 AEGDWKAAAGLVRLKVMGAGLPGGTSFMEDYTYHLTPGNELVLGAHMLEVCPTIAKEKPR 360
Db 301 AEGDWKAAAGLVRLKVMGAGLPGGTSFMEDYTYHLTPGNELVLGAHMLEVCPTIAKEKPR 360

QY 361 IEVHPLSIGGKADPARLVFDQEGPAPVNASIVDMGNRFRLLVNRVLSVPIERKMPKLPTA 420
Db 361 IEVHPLSIGGKADPARLVFDQEGPAPVNASIVDMGNRFRLLVNRVLSVPIERKMPKLPTA 420

QY 421 RVLWKPLPDFKRATTAWILAGGSHHTAFSTAVDVEYLIDWAEALEIEYLVIDENLDLENF 480
Db 421 RVLWKPLPDFKRATTAWILAGGSHHTAFSTAVDVEYLIDWAEALEIEYLVIDENLDLENF 480

QY 481 KKELRWNELYWGLLKR 496
Db 481 KKELRWNELYWGLLKR 496
```

```

RESULT 3
US-10-193-896-11
; Sequence 11, Application US/10193896
; GENERAL INFORMATION:
; APPLICANT: Biotechnologisk Institut
; APPLICANT: Jorgensen, Flemming
; APPLICANT: Hansen, Ole C.
; APPLICANT: Stougaard, Peter
; APPLICANT: Berthelsen, Hans
; APPLICANT: Eriknauer, Kristian
; APPLICANT: Botcher, Karen
; APPLICANT: Christensen, Hans Jorgen Singel
; TITLE OF INVENTION: A novel thermostable isomerase and use
; FILE REFERENCE: 30077US02
; CURRENT APPLICATION NUMBER: US/10/193,896
; CURRENT FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/305,155
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/905,108
; PRIOR FILING DATE: 2001-07-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 496
; TYPE: PRT
; ORGANISM: T.maritima
```

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OM protein - protein search, using sw model

Run on: October 18, 2004, 22:37:36 ; Search time 42' Seconds
(without alignments)
1136.274 Million cell updates/sec

Title: US-10-600-689-4
Perfect score: 2612
Sequence: 1 MIDLKQYEFWFLVGSQYLYG.....LENFKKELRWNELYWGLLKR 496

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum_DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2508	96.0	496	2 B72398	L-arabinose isomer
2	1547	59.2	497	2 A83884	L-arabinose isomer
3	1445.5	55.3	500	2 AC0515	L-arabinose isomer
4	1443.5	55.3	500	1 ISEBAB	L-arabinose isomer
5	1436.5	55.0	500	1 ISECAB	L-arabinose isomer
6	1435.5	55.0	500	2 B85488	L-arabinose isomer
7	1435.5	55.0	500	2 B90637	L-arabinose isomer
8	1424.5	54.5	498	2 C69587	L-arabinose isomer
9	1424.5	54.5	500	2 AE0274	L-arabinose isomer
10	1301	49.8	488	2 G97065	L-arabinose isomer
11	1270	48.6	488	2 C97065	L-arabinose isomer
12	137	5.2	471	2 B72314	hypothetical prote
13	127.5	4.9	475	2 H95997	probable L-arabino
14	117	4.5	1481	1 QZDOP3	pyrimidine synthes
15	115	4.4	467	2 AG1203	hypothetical prote
16	112	4.3	608	2 G81397	hsp90 family heat
17	106.5	4.1	1651	2 F88750	protein vit-6 limp
18	106.5	4.1	1651	2 B43081	vitellogenin vit-6
19	106	4.1	328	2 F81005	probable proteinas
20	106	4.1	1613	2 G64488	reverse gyrase (in
21	105.5	4.0	320	2 F75063	hypothetical prote
22	105	4.0	2201	2 A32160	tenascin-C - human
23	105	4.0	4466	1 S17231	dynein beta heavy
24	104.5	4.0	2242	2 A57541	pyrimidine synthes
25	104	4.0	328	2 H82025	probable proteinas
26	104	4.0	1246	2 JQ0406	hypothetical prote
27	103.5	4.0	815	2 E70021	3-hydroxyacyl-CoA
28	103	3.9	872	2 S76197	endopeptidase Clp
29	103	3.9	1152	2 AC1347	probable peptidogl

ALIGNMENTS

RESULT 1

B72398

L-arabinose isomerase - Thermotoga maritima (strain MSB8)

C;Species: Thermotoga maritima

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C;Accession: B72398

R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hicke

Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.

C.M.

Nature 399, 323-329, 1999

A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome se

A;Reference number: A72200; MUID:99287316; PMID:10360571

A;Accession: B72398

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-496 <ARN>

A;Cross-references: UNIPROT:Q9WYB3; GB:AE001709; GB:AE000512; NID:g4980763; PIDN:AAD353

A;Experimental source: strain MSB8

C;Genetics:

A;Gene: TM0276

C;Superfamily: L-arabinose isomerase

Query Match	96.0%;	Score 2508;	DB 2;	Length 496;
Best Local Similarity	94.8%;	Pred. No. 4.3e-169;		
Matches 470;	Conservative 18;	Mismatches 8;	Indels 0;	Gaps 0;
QY	1	MIDLKQYEFWFLVGSQYLYGLET	KKVEQQASRIVEALNNDPIF	PSKIVLKPVLKNSAEI 60
Db	1	MIDLKQYEFWFLVGSQYLYGLET	KKVEQQASKIVDSLND	DDPIFPSKIVLKPVLKSSSEI 60
QY	61	REIFEKANAEPKCAGVIVMHTF	SPSKMWIRGLSINKKPL	LLHLHTQYNREIPWDTIDMDY 120
Db	61	TEIFEKANADPKCAGVIVMHTF	SPSKMWIRGLSINKKPL	LLHLHTQYNREIPWDTIDMDY 120
QY	121	MNLNQSAGHDREHGFHARMRL	PRKVVVGHWDREVREKIA	KWMRVACAIQDGRGTQIVR 180
Db	121	MNLNQSAGHDREHGFHARMRL	PRKVVVGHWEKEVREKIA	KWMRVACAIQDGRMGQIVR 180
QY	181	FGDNMREVASTEDDKVEAQIK	LGWSINTGWVGELAE	GVKAVPENEVEELLKEYKERYIMP 240
Db	181	FGDNMREVASTEGDKVEAQIK	LGWSINTGWVGELAE	RVKAVPEREVEELLKEYREKYIMP 240
QY	241	EDEYSLKAIREQAKMEIALRE	FLKEKNAIAFTTTFFED	LHDLPLQPLGLAVQRLMEEGYGF 300
Db	241	EDEYSLKAIREQAKIEIALRE	FLKEKNAVGTTF	FEDLHDLPLQPLGLAVQRLMEEGYGF 300
QY	301	AEGDWKAAGLVRAALKVMGAG	LPGGTSFMEDYTYHLT	PGNELVLGAHMLEVCPTIAKEKPR 360
Db	301	AEGDWKAAGLVRAIKVMGTSL	PGGTSFMEDYTYHLT	PGNELVLGAHMLEVCPTIAKEKPR 360
QY	361	IEVHPLSIGGKADPARLVFD	GOEGPAVNASIVDMGN	RFLVVRVLSVPIERKMPKLPTA 420

Db 361 IEVHPLSIGGKADPARLVFDGQEGPAVNASIVDMGNRFRLLVNVKLVSVPIERKMPKLPFTA 420

Qy 421 RVLWKPLPDFKRAATTAWILAGSGSHHTAFSTAVDVEYLIDWAEALEIEYLVIDENLDLENF 480

Db 421 RVLWKPLPDFKRAATTAWILAGSGSHHTAFSTAVDVEYLIDWAEALEIEYVVIDENLDLED 480

Qy 481 KKELRWNELYWGLLKR 496

Db 481 KKELRWNELYWGLLKR 496

RESULT 2

A83884

L-arabinose isomerase araA [imported] - Bacillus halodurans (strain C-125)

C;Species: Bacillus halodurans

C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004

C;Accession: A83884

R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira

Nucleic Acids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A;Reference number: A83650; MUID:20512582; PMID:11058132

A;Accession: A83884

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-497 <STO>

A;Cross-references: UNIPROT:Q9KBQ2; GB:AP001513; GB:BA000004; NID:g10174345; PIDN:BAB055

A;Experimental source: strain C-125

C;Genetics:

A;Gene: araA

C;Superfamily: L-arabinose isomerase

Query Match 59.2%; Score 1547; DB 2; Length 497;

Best Local Similarity 58.6%; Pred. No. 2.5e-101;

Matches 293; Conservative 72; Mismatches 127; Indels 8; Gaps 3;

Qy 1 MIDLKQYEFWFLVGSQYLYGLETLLKKVEQASRIVEALNNDPIPPSKIVLKPVLKNSAEI 60

Db 1 MLQTKPYTFWITSQHLYGEDAIEQVRQHSQTMVEKLNKIGELPYTIELKEVLTTPDAI 60

Qy 61 REIFEKANAEPCAGVIVVMHTFSPSKMIRGLSINKKPLLHLHTQYNREIPWDTIDMDY 120

Db 61 RKMVIAANSDDDCAGMITWMHTFSPAKMWINGLKQKKPLLHLHTQFNREIPYDDIDMDF 120

Qy 121 MNLNQSAGHDREHGFHARMRLPRKVVVGHWDREVREKIAKWMRVACAIODGRTGQIVR 180

Db 121 MNLNQSAGHDREYGHIGARLNISRKVIIVGHWNQNDVQERLGAWMTAAAFVDGHHLKVAR 180

Qy 181 FGDNMREVASTEDDKVEAQIKLGWSINTWVGELAEGVKAVPENEVEELLKEYKERY --- 237

Db 181 FGDNMREVAVTEGDKVEAQIQFGWSITAFGIGDLVEKMKAVSEDEVRRLLFDEYQELYRLS 240

Qy 238 --IMPEDEYSLKAIREQAKMEIALREFLKEKNAIAFTTTTFEDLHDLPLQPLGLAVQRLMEE 295

Db 241 PSILEQDEVK-AAVLEQAKMELALKEFLEEGGYTAFTTNFEDLHGMKQLPGLAVQRLMAE 299

Qy 296 GYGFGAEGDWKAAGLVRLKVMGAGLPGGTSFMEDYTYHLTPGNELVLGAHMLVCPPTIA 355

Db 300 GYGFGGEGDWKTAALLRMKIIADG--KGTSMEDYTYHLAEGNELVLGSHMLEICPTIA 357

Qy 356 KEKPRIEVHPLSIGGKADPARLVFDGQEGPAVNASIVDMGNRFRLLVNVRLSVPIERKMP 415

Db 358 ANQPEIQVHPLGIGGKEDPARLVFDGADGAPALNASLIDLGHFRFLVNEVEAIKPERDMP 417

Qy 416 KLPTARVLWKPLPDFKRAATTAWILAGSGSHHTAFSTAVDVEYLIDWAEALEIEYLVIDENL 475

Db 418 KLPVAKVLWKCKPSLSEATEAWIHAGGAHHTVFSFEVTPTEQLYDWTATLADIEVVFINDKT 477

Qy 476 DLENFKKELRWNELYWGLLK 495

Db 478 DVLQFQOQLQWNEAFRRLLFK 497

RESULT 3

AC0515

L-arabinose isomerase [imported] - Salmonella enterica subsp. enterica serovar Typhi (st

C;Species: Salmonella enterica subsp. enterica serovar Typhi

A;Note: this species has also been called Salmonella typhi

C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C;Accession: AC0515

R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,

th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,

, S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.

A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov

A;Reference number: AB0502; MUID:21534947; PMID:11677608

A;Accession: AC0515

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-500 <PAR>

A;Cross-references: GB:AL513382; PIDN:CAD01259.1; PID:g16501387; GSPDB:GN00176

C;Genetics:

A;Gene: STY0119

C;Superfamily: L-arabinose isomerase

Query Match 55.3%; Score 1445.5; DB 2; Length 500;

Best Local Similarity 55.1%; Pred. No. 3.6e-94;

Matches 271; Conservative 82; Mismatches 134; Indels 5; Gaps 3;

Qy 7 YEFWFLVGSQYLYGLETLLKKVEQASRIVEALNNDPIPPSKIVLKPVLKNSAEIRIFEK 66

Db 7 YEVWFVIGSQHLYGAETLRQVTHAEHVVNALNTEAKLPCKLVLPGLTSPDEITATCRD 66

Qy 67 ANAEPKACGIVIVVMHTFSPSKMIRGLSINKKPLLHLHTQYNREIPWDTIDMDYMNLNQS 126

Db 67 ANYDDRCAGLVVWLHTFSPAKMWINGLSILNKPQLQHTQFNAALPWDSIDMDFMNLNQT 126

Qy 127 AHGDREHGFHARMRLPRKVVVGHWDREVREKIAKWMRVACAIODGRTGQIVRFGDNMR 186

Db 127 AHGREGFGFIGARMRQOHAVVTGHWQDKEAHTRIGAWMRQAVSKQDTRQLKVCVCFGDNMR 186

Qy 187 EVASTEDDKVEAQIKLGWSINTWVGELAEGVKAVPENEVEELLKEYKERY-IMPEDEY- 244

Db 187 EVAVTDGDKVAAQIKFGFSVNTWAVGDLVQVVNSIGDGDISALIDEYESSYTLTPATQIH 246

Qy 245 --SLKAIREQAKMEIALREFLKEKNAIAFTTTTFEDLHDLPLQPLGLAVQRLMEEGYGFGE 302

Db 247 GDKRONVREAARIELGMKRFLEGGFHAFTTTTFEDLHGLKQLPGLAVQRLMOQGYGFAGE 306

Qy 303 GDWKAAGLVRLKVMGAGLPGGTSFMEDYTYHLTPGNELVLGAHMLVCPPTIA-KEKPRI 361

Db 307 GDWKTAAALLRIMKVMSTGLQGGTSFMEDYTDHFEKGNLVLGSHMLEVCPSTIAVEEKPIL 366

Qy 362 EVHPLSIGGKADPARLVFDGQEGPAVNASIVDMGNRFRLLVNVRLSVPIERKMPKLPAR 421

Db 367 DVQHLGIGGKEDPARLIFNTQTGPAIVASLIDLGDRLVLLVNCIDTVKTPHSLPKLPVAN 426

Qy 422 VLWKPLPDFKRAATTAWILAGSGSHHTAFSTAVDVEYLIDWAEALEIEYLVIDENLDLENFK 481

Db 427 ALWKAQPDLPPTASEAWILAGGAHHTVFSHALDNDMRQFAEIHDIETAVIDNDTRLPAFK 486

Qy 482 KELRWNELYWGL 493

Db 487 DALRWNEVYYGL 498

RESULT 4

ISEBAB

L-arabinose isomerase (EC 5.3.1.4) - Salmonella typhimurium

C;Species: Salmonella typhimurium

C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004

C;Accession: A24985

R;Lin, H.C.; Lei, S.P.; Wilcox, G.

Gene 34, 123-128, 1985

A;Title: The araBAD operon of Salmonella typhimurium LT2. II. Nucleotide sequence of ara

A;Reference number: A24985; MUID:85232045; PMID:3891513